Original Research Article

GeneticalContributions andCombining Ability Analysis in Bitter gourd (*Momordicacharantia* L.)

Abstract

The present study was undertaken to estimate the general and specific combining ability in 10 x 10 diallel set of crosses (excluding reciprocals) in bitter gourd to get 45 hybrids using 10 parents (DVBTG-1, VRBT-94, VRBT-39, VRBT-41, VRBT-49, VRBT-50, VRBT-103, VRBT-63, VRBT-32 and VRBT-6). These 45 F_1 along with 10 parents were evaluated in Randomized Block Design with three replications considering 10 characters (days to first male flower anthesis, days to first female flower anthesis, days to first harvest, number of branches/plant, plant height, fruit length, fruit diameter, number of fruits/plant, fruit weight and fruit yield/plant) in bitter gourd.Analysis of variance due to treatment was highly significant for all the traits. The combining ability analysis revealed highly significant differences among the treatments for all the parameters studied. The variances due to sca were higher than the gca for all the characters indicating the predominance of non-additive gene effects. Out of 10 parents' four parents DVBTG-1, VRBT-49, VRBT-103 and VRBT-32 exhibited significant and positive g.c.a effects for early female flowering and days to first harvest. Similarly, positive and significant g.c.a effects were shown by DVBTG-1, VRBT-50, VRBT-49, VRBT-103 and VRBT-6 for number of fruits/plant. DVBTG-1 and VRBT-49 were identified as consistent best general combiners for fruit yield and other components. The cross combinations VRBT-94 x VRBT-32, DVBTG-1 x VRBT-50, VRBT-49 x VRBT-103, VRBT-49 x VRBT-32, VRBT-94 x VRBT-32 and VRBT-41 x VRBT-103 exhibited positive and significant s.c.a effects for first female flower anthesis and days to first harvest. The finding of experiments confirmed the potentiality of DVBTG-1 x VRBT-6, VRBT-94 x VRBT-103, VRBT-41 x VRBT-6, VRBT-94 x VRBT-49, VRBT-39 x VRBT-49 and VRBT-94 x VRBT-39 combination based hybrids for yield/plant. The results of this study also suggest that for improvement of a desirable character, the selected parental line should be of high gca value and their F_1s should express high specific combining ability.Significant estimates of additive component (d) along with significance odadditive x additive (i) gene interactionwithpositive sign pod yield per plant which indicated the presence of increase alleles and associated pair of genes.

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Key words: Bitter gourd, diallel analysis, Genetical contributions, GCA, SCA, quantitative traits

Introduction

Bitter gourd (*Momordicacharantia* L.) is an important cucurbit, which is grown throughout the countryfor its nutritious vegetable. Reader's Digest UK recently featured bitter gourd as one of the "Five Foods that Will Save the World" along with scuba rice, mungbean, disease-resistant banana, and drought-hardy maize. Bitter gourd is well known for nutritional, medicinal (antidiabetic) and other curative properties and due to these properties, tender green fruits have captured a prominent position among vegetables. It is now an export oriented vegetable which is generally marketed in fresh but sometimes in dehydrated or osmo-drying form. It is one of the most popular vegetables in China, Taiwan, Vietnam, Thailand, India and the Philippines (Xiang *et al.*, 2000). Occurrence and distribution of both wild and cultivated forms of bitter gourd indicates its rich diversity in India (Pandey *et al.*, 2019). The predominant sex form in bitter gourd is monoecious, howevergynoecious sex form (only female flower bearing plant) has been reported from India, Japan and China (Ram *et al.*, 2002; Zhou *et al. 1998;* Ram *etal*. 2006; Behera*et al*. 2006; Iwamoto and Ishida 2006).In the past few years, due to several factors such as incidence of viral diseases like leaf mosaic virus and unavailability of good quality and pure seeds of desired types, there is drastic reduction in yield potential, even in some popular varieties like PDM, ArkaHarit, MC-84 etc. are worse affected. Choice of parents is considered an important aspect in any breeding programme aimed in improving yield and its related attributes because the high yielding parent may not necessarily transfer its superiority to the progenies in the crosses. Commonly, gca and sca effects have been extensively used in breeding programme to identify the desirable parents and crosses. Hence the present study was undertaken to assess the combining ability and to determine the nature and magnitude of genetic variances for yield and yield contributing traits in bitter gourd.

MATERIALS AND METHODS

The experiment was conducted at ICAR-Indian Institute of Vegetable Research, Varanasi (U.P.). In the present investigation, the experimental materials used for the study comprised of 10 genetically diverse inbred lines viz. DVBTG-1, VRBT-94, VRBT-39, VRBT-41, VRBT-49, VRBT-50, VRBT-103, VRBT-63, VRBT-32 and VRBT-6 and 45 hybrids (F_{1s})developed through half-diallelmating design. The experiment was laid down with 10 parents and 45 F_{1s} hybrids in a Randomized Block Design (RBD) with three replications. In each row seeds were sown keeping row to row and plant to plant spacing of 60 cm x 45 cm., respectively. All the recommended agronomic and cultural practices were adopted to ensure a good crop. Observations were recorded on 5 randomly selected plants from each of parents and crosses in each replication on 10 characters (days to first male flower anthesis, days to first female flower anthesis, days to first harvest, number of branches/plant, plant height, fruit length, fruit diameter, number of fruits/plant, fruit weight and fruit yield/plant) in bitter gourd. The estimates of combining ability variances and effects were obtained using method 2 of model-1 Griffing (1956a).

Result and Discussion

With the advancement in biometrical genetics, several techniques are now available which permit quantitative genetic analysis and selection of promising parents crosses for further exploitation. The parents who produced good progenies upon crossing are of immense value to the plant breeder. In a crop improvement programme, success depends upon the isolation of valuable cross combinations as determined in the form of parents with high combining ability. The emphasis is on the importance of testing the combining ability of parents because many times the high yielding parents may not combine well to give good segregates.Combining ability analysis is a powerful tool to identify inbreds having good potential to transmit the desirable traits to their off-springs and also helps in sorting out promising crosses for fruit yield and its attributes. At the same time, it also elucidates the nature of gene action (additive and non-additive) involved in the inheritance.

***Analysis of variance*:**

Analysis of variances for diallel progenies for 10 characters in bitter gourd revealed vast diversity which contributes significantly in development of various cross combinations in bitter gourd. The value indicates the parent's utility for earliness, total yield and other yield related traits. Analysis of variances for combining ability with respect to different characters is presented in table 1.The analysis of variance revealed significant among the parents for the characters under study. The difference between parents found significant for all the characters, indicating that the parents differed significantly for these characters.

Genetical Contribution

The total variability among F_1 hybrids was further portioned into different components and their significance was tested. It is evident from the table-2 that the mean sum of squares due to crosses was significant for all ten characters studied (Ram *et al*., 1999). The character under study indicated the importance of both additive and non-additive genetic components which is corroborated with the findings of Ram *et al*. (1997).The relative role of gene action was in general more complex for yield and other associated traits. The nature and magnitude of gene effects vary with different cross/character-wise. Further, duplicate type of epistasis was also found in majority of traits in one or the other cross combinations. In such crosses, the selection intensity should be mild in the earlier and intense in the later generations because it marks the progress through selection.

General combining ability effects: Positive and significant gca effects were observed by parents DVBTG-1, VRBT-32, VRBT-50 and VRBT-103 for first male flower anthesis, female flower anthesis and days to first harvest (table-4). The estimates of gca effects (table 3) showed that parents DVBTG-1(3.26) and VRBT-32 (2.87) were good general combiner for male flower anthesis, VRBT-63 (-2.57). Parent VRBT-41 (0.53) and VRBT-6 (0.63) found significant for plant height. Significant and negative gca effects were shown by VRBT-94 (-0.40), VRBT-63 (-0.38) and VRBT-6 (0.63) which indicate reduction in plant height. Parent VRBT-94 (1.57), VRBT-39 and VRBT-49 (0.66) showed positive effects for number of branches/plant whereas DVBTG-1 (-0.76) expressed negative value towards this trait. Parent VRBT-41, VRBT-50, VRBT-6, VRBT-32 and VRBT-6 were noted good general

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Comment [G12]: Two times mentioned here combiners. Positive and significant gca effects were exhibited by VRBT-50 (347.1), VRBT-6 (250.75) and VRBT-94 (120.82) for yield/plant and found good general combiners for this trait. It was observed that performance of parents bear direct relation for their respective gca effects in the parents which showed highest gca effects for different character were also observed good performers with respect to that particular character. Above findings are very much similar to the results put forth by Ram *et al.* (1999).

Specific combining ability effects: Since in the present study, the magnitude of non-additive variances were higher, the per se performance may not be real indicative for their gcaeffects (table-5). Hence the sca effects were also calculated. The estimates of sca effects (table 5) revealed that crosses VRBT-94 x VRBT-6, DVBTG-1 x VRBT-50, VRBT-49 x VRBT-32, VRBT-49 x VRBT-103 and VRBT-41 x VRBT-103 combine well to produce significant negative sca effects being desirable for days to male, female anthesis and days to harvesting. High positive sca effects were observed in cross combinations VRBT-39 x VRBT-32, VRBT-41 x VRBT-32, VRBT-39 x VRBT-63, DVBTG-1 xVRBT-50, VRBT-94 x VRBT-32 but significant and high negative sca effects found in cross combinations VRBT-94 x VRBT-6, VRBT-39 x VRBT-50, VRBT-50 x VRBT-32, VRBT-50 x VRBT-6 and VRBT-41 x VRBT-50 indicating poor specific combination for plant height. Similarly the crosses VRBT-49 x VRBT-50, VRBT-49 x VRBT-6, VRBT-94 x VRBT-32, VRBT-94 x VRBT-41, VRBT-41 x VRBT-32, VRBT-39 x VRBT-32 and VRBT-50 x VRBT-63 expressed significant sca effects for number of branches/plant. For fruit length highly positive and significant sca effects were noted in the cross combinations VRBT-49 x VRBT-50, VRBT-50 x VRBT-63, DVBTG-1 x VRBT-6, VRBT-49 x VRBT-103, VRBT-103 x VRBT-6, VRBT-94 x VRBT-6 and VRBT-41 x VRBT-32. Highly positive and significant sca effects were noted in the cross combinations DVBTG-1 x VRBT-6, VRBT-94 x VRBT-103, VRBT-41 x VRBT-6, VRBT-94 x VRBT-49, VRBT-39 x VRBT-49 and VRBT-94 x VRBT-39 but combinations VRBT-49 x VRBT-32, VRBT-94 x VRBT-50, DVBTG-1 x VRBT-39, VRBT-39 x VRBT-103, VRBT-49 x VRBT-63 and DVBTG-1 x VRBT-94 gave significant and highly negative sca effects indication poor specific combination for this trait Ram *et al.* (1999) and Mishra *et al.* (2012).

Most of the crosses included high x high and high x medium type of general combiners. The desirable cross combination with medium x medium and poor x poor type of general combiners also observed which may be due to complimentary effects. The crosses involving parents with good gca effects can be exploited effectively by conventional breeding procedure like pedigree method. However, the crosses involving good combiner and other medium poor combiner could produce desirable transgressive segregants if additive genetic system was operative good combining parents and epistatic effect also act in the same direction. Similar results were also reported by Singh et al. (2013), Shukla et al. (2014),Laxuman et al. (2012) and Mishra et al. (2012).

It is suggested that it would be desirable to follow cyclic method of breeding for combining superior recombinants which will simultaneously exploit additive and non-additive gene effects for evolving the desirable genotypes.

Table.1. Analysis of variances for diallel progenies for 10 characters in bitter gourd

Source	df	1st male flower anthesis	1st female flower anthesis	Days to 1st harvesting	Plant height (m)	No. of branches/ plant	Fruit length (cm)	Fruit diameter (cm)	No. of fruits/plant	Av. fruit wt. (g)	Yield/plant (g)
Treatment	99	68.94**	68.44**	65.51**	2.84**	62.42**	23.73**	1.11**	104.88**	505.18**	938626.43**
Parent	9	92.63**	86.30**	86.92**	1.51**	21.75**	14.01**	1.05**	22.51**	256.67**	179377.18**
F_1	44	57.14**	54.78**	57.22**	2.01**	45.71**	12.62**	0.99**	54.79**	752.51**	669459.71**
PVF_1	1	439.88**	677.97**	762.63**	33.99**	844.38**	616.28**	8.78**	2822.09**	9209.69**	264280.46**
Replication	2	50.57	58.71	62.41	0.43	1.48	0.09	0.03	0.56	5.34	2918.74
Error	198	1.11	1.27	1.82	0.06	0.75	0.11	0.05	0.35	2.92	2523.69

*, ** = Significant at 5% and 1% level of probability, respectively

Table.2. Genetical contribution in F_1 progenies under diallel for 10 characters in bitter gourd

Components	1st male flower anthesis	1st female flower anthesis	Days to 1st harvesting	Plant height (m)	No. of branches/ plant	Fruit length (cm)	Fruit diameter (cm)	No. of fruits/ plant	Av. fruit wt. (g)	Yield/plant (g)
D	30.5**	28.34**	28.37**	0.48	7.00	4.63**	0.33**	7.39	84.58*	59040.70
	(+7.03)	(+5.44)	(+6.05)	(+0.21)	(+4.52)	(+0.38)	(+0.09)	(+6.81)	(+30.94)	(56158.86)
H_1	314.63**	294.68**	309.4**	11.00**	288.09**	56.93**	6.03**	386.27**	1671.50**	2039345.10**
	(+59.81)	(+46.29)	(+51.50)	(+1.77)	(+38.47)	(+3.20)	(+0.78)	(+58.00)	(+263.40)	(+478157.52)
H_2	362.84**	260.56**	280.2**	9.53**	271.19**	54.01**	4.75**	367.69**	1361.71**	1824487.08**
	(+50.59)	(+39.34)	(+43.77)	(+1.50)	(+32.70)	(+2.72)	(+0.66)	(+49.30)	(+223.86)	(+406380.84)
h^2	57.93**	89.34**	100.45**	4.48**	111.37**	81.34**	1.15**	372.47**	1215.33**	618343.65**
	(+8.52)	(+6.58)	(+7.32)	(+0.25)	(+5.47)	(+0.45)	(+0.11)	(+8.25)	(+37.46)	(+68003.89)

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F	59.24	45.93	44.23	0.64	14.60	-4.05*	0.96	-4.15	-107.42	-95487.01
	(+32.46)	(25.09)	(+27.91)	(+0.96)	(+20.85)	(1.73)	(0.42)	(+31.44)	(142.76)	(+259150.77)
E	0.37	0.42	0.61	0.020	0.25	0.04	0.02	0.12	0.98	751.45
	(+2.12)	(+1.64)	(+1.82)	(+0.06)	(1.36)	(+0.11)	(0+0.03	(+2.05)	(+9.33)	(+16932.53)
$(H1/D)^{1/2}=F_1$	3.21	3.22	3.30	4.77	6.42	3.51	4.25	7.23	4.45	5.88
$H_2/4H_1$	0.21	0.22	0.23	0.22	0.24	0.24	0.20	0.24	0.20	0.22
KD/KR	1.87	1.67	1.62	1.32	1.39	0.78	2.02	0.93	0.75	0.76
h^2/H_2	0.22	0.34	0.36	0.47	0.41	1.51	0.24	1.01	0.89	0.34
r	0.6794*	0.7336*	0.7863*	-0.5518	-0.5400	+0.9598*	+0.3179	+0.7514*	-0.5090	0.2164
t^2	0.4286	0.5134	0.6413	0.2503	0.3833	0.5379	0.3113	3.4106**	0.9548	21.4566**
Heritability (NS)	37.65	35.11	32.97	16.17	9.62	22.01	23.45	6.94	15.01	9.53

*, **= Significant at 5% and 1% level of probability, respectively

Table.3. The analysis of variance for GCA and SCA under diallel mating design for 10 characters

Characters	***df***	**GCA**		**SCA**		**Error**		**GCA/SCA**	
		F_1	**F_2**	**F_1**	**F_2**	**F_1**	**F_2**	**F_1**	**F_2**
First male flower anthesis	45	44.167**	32.03**	19.227**	23.461**	0.371	0.313	2.297	1.365
First female flower anthesis	45	45.679**	31.167**	19.494**	24.085**	0.422	0.408	2.343	1.294
Days to first harvesting	45	45.420**	29.502**	21.008**	24.285**	0.607	0.609	2.162	1.215
Plant height (m)	45	1.431**	0.923**	0.751**	0.849**	0.020	0.019	1.905	1.087
No. of branches/plant	45	11.723**	31.659**	20.258**	19.543**	0.251	0.260	0.579	1.619
Fruit length (cm)	45	20.508**	23.478**	5.512**	31.491**	0.037	24.314	3.721	0.746
Fruit diameter (cm)	45	0.478**	0.375**	0.361**	0.323**	0.015	0.0015	1.324	1.161
No. of fruits/plant	45	37.104**	60.050**	32.841**	27.572**	0.117	0.158	1.129	2.178
Average fruit weight (g)	45	55.00**	284.487**	122.815**	63.190**	0.976	0.885	4.478	4.502
Yield/plant (g)	45	5801.97**	4088.54**	3098.78**	1345.93**	841.972	751.449	1.872	3.039

Table.4. Estimates of general combining (gca) ability effects for various traits in bitter gourd

Genotype	First male flower anthesis	First female flower anthesis	Days to first harvesting	Plant height (m)	No. of branches /plant	Fruit length (cm)	Fruit diameter (cm)	No. of fruits/plant	Average fruit weight (g)	Yield/plant (kg)
DVBTG-1	3.26	3.46**	3.54**	-0.23**	-0.76**	-0.34**	0.15**	0.85**	-1.13**	15.54**
VRBT-94	-0.61**	-0.87**	-1.07**	-0.40**	1.57**	-0.04*	0.02	1.76**	-0.22**	120.82**
VRBT-39	0.71*	0.27**	0.23*	0.03*	-0.20**	-1.05**	0.29**	1.8**	-1.28**	81.04**
VRBT-41	-0.74**	-0.96**	-0.77**	0.53**	0.64**	-0.91**	0.15**	0.06	1.65**	60.11**
VRBT-49	-0.33**	-0.15**	0.15	-0.15**	0.66**	-0.61**	-0.26	-1.06**	-4.62**	-136.68**
VRBT-50	0.28**	-0.09	-0.38**	0.04*	0.22**	2.04**	0.08**	1.79**	10.98**	347.11**
VRBT-103	0.20**	0.27**	0.23*	-0.10**	-1.94**	-1.28**	-0.20**	0.29**	-6.57**	-115.23**
VRBT-63	-2.80**	-2.57**	-2.35**	-0.38**	-0.79**	-1.39**	0.04**	-2.35**	-6.46**	-296.65**
VRBT-32	2.87**	2.93**	2.84**	0.03*	-0.08	-0.46**	-0.33**	-3.28**	-4.86**	-326.81**
VRBT-6	-2.30**	-2.29**	-2.43**	0.63**	0.67**	2.23**	0.07**	0.13**	12.51**	250.75**
SE (gi)	0.0556	0.0593	0.0711	0.0130	0.045	0.0175	0.0112	0.0312	0.0901	2.6490
SE (gi-gj)	0.0375	0.0399	0.0479	0.0009	0.0308	0.0118	0.0008	0.0210	0.0607	1.7860

*, **= Significant at 5% and 1% level of probability, respectively

Table.5. Specific combining abilityeffects for various traits in the F_1 generation of bitter gourd

Crosses	**First male flower anthesis**	**First female flower anthesis**	**Days to first harvesting**	**Plant height (m)**	**No. of branches/plant**	**Fruit length (cm)**	**Fruit diameter (cm)**	**No. of fruits/ plant**	**Average fruit weight (g)**	**Yield/ plant (kg)**
DVBTG-1 x VRBT-94	-0.89**	-1.39**	-2.61**	-1.15**	1.55**	0.35**	0.35**	-1.48**	-1.48**	-197.50**
DVBTG-1 x VRBT-39	2.00**	1.81**	1.09**	-0.04**	-2.22**	0.47**	0.27**	-1.19**	-3.31**	-260.89**
DVBTG-1 x VRBT-41	-4.41**	-4.31**	-4.91**	0.62**	1.31**	1.57**	-0.68**	3.42**	-1.28**	198.11**
DVBTG-1 x VRBT-49	-8.16**	-6.78**	-7.16**	0.47**	4.39**	0.02	-0.10**	0.01	-1.32**	-106.34**
DVBTG-1 x VRBT-50	6.56**	5.83**	6.7**	1.08**	5.5**	1.7**	0.19**	1.89**	15.89**	465.77**
DVBTG-1 x VRBT-103	-0.03	0.81**	2.09**	0.83**	3.82**	0.39**	0.33**	3.06**	-1.76**	137.52**
DVBTG-1 x VRBT-63	-2.69**	-4.03**	-3.99**	-0.29**	-2.56**	-0.13**	0.66**	-0.43**	-4.80**	-137.13**
DVBTG-1 x VRBT-32	-5.36**	-4.86**	-4.52**	-0.74**	-3.37**	2.04**	-0.60**	2.5**	5.36**	338.49**
DVBTG-1 x VRBT-6	-4.86**	-4.97**	-4.91**	0.40**	-1.82**	2.21**	0.06**	6.08**	18.16**	960.40**
VRBT-94 x VRBT-39	-2.14**	-2.86**	-2.63**	0.56**	1.89**	1.29**	0.91**	3080**	7.71**	501.63**
VRBT-94 x VRBT-41	2.45**	2.69**	2.37**	0.79**	6.65**	1.33**	0.52**	-1.93**	7.44**	-16.63**
VRBT-94 x VRBT-49	-3.64**	-4.11**	-4.22**	0.27**	-1.63**	0.02	0.22**	8.16**	4.17**	597.41**
VRBT-94 x VRBT-50	2.75**	2.5**	1.98**	-0.35**	-3.69**	0.96**	-0.12**	-5.39**	6.68**	-296.98**

VRBT-94 x VRBT-103	-2.83**	-3.53**	-3.97**	-0.64**	-3.30**	-0.28**	-0.40**	10.31**	1.99**	685.74**
VRBT-94 x VRBT-63	-2.16**	-2.36**	-2.38**	0.54**	5.19**	2.5**	0.26**	5.05**	7.95**	517.69**
VRBT-94 x VRBT-32	3.84**	3.14**	3.09**	1.00**	6.87**	-0.63**	-0.74**	4.35**	0.31**	280.71**
VRBT-94 x VRBT-6	7.34**	6.69**	7.03**	-1.54**	-5.51**	1.77**	0.53**	-0.13**	14.28**	269.36**
VRBT-39 x VRBT-41	-1.00**	-1.78**	-1.94**	0.03	3.15**	0.85**	-0.16**	-0.43**	0.14	-73.20**
VRBT-39 x VRBT-49	0.59**	0.08	0.14**	-0.19**	-1.87**	1.24**	-0.35**	7.92**	3.7**	551.29**
VRBT-39 x VRBT-50	2.31**	2.03**	1.67**	-1.04**	-3.69**	1.88**	0.61**	-0.23**	8.48**	177.73**
VRBT-39 x VRBT-103	-5.61**	-6.00**	-5.94**	0.14**	1.16**	0.37**	-0.31**	-2.66**	-0.07	-201.83**
VRBT-39 x VRBT-63	-0.94**	-1.83**	-2.69**	1.09**	2.09**	-0.38**	0.55**	6.51**	-2.55**	352.83**
VRBT-39 x VRBT-32	0.72**	-0.33**	0.45**	1.58**	5.87**	062**	-0.84**	3.68**	0.45**	258.65**
VRBT-39 x VRBT-6	1.22**	0.89**	1.06**	0.64**	3.69**	0.96**	-0.48**	3.76**	-0.55**	302.86**
VRBT-41 x VRBT-49	-0.50**	-1.03**	-0.52**	0.71**	-3.97**	0.87**	0.53**	4.36**	4.27**	340.06**
VRBT-41 x VRBT-50	-4.11**	-4.42**	-3.66**	-0.81**	-1.53**	0.05	-0.54**	4.14**	-4.36**	262.23**
VRBT-41 x VRBT-103	4.64**	3.89**	4.06**	0.06**	2.42**	0.68**	0.48**	0.98**	-0.58**	22.51**
VRBT-41 x VRBT-63	-1.36**	2.06**	2.64**	-0.09**	-3.15**	-0.54**	-0.31**	0.02	-5.65**	-143.40**
VRBT-41 x VRBT-32	-0.03	-0.78**	-1.88**	1.13**	6.27**	1.76**	1.07**	2.82**	11.78**	384.12**
VRBT-41 x VRBT-6	-3.53**	-3.89**	-3.61**	0.03	-2.89**	1.00**	0.37**	4.67**	12.64**	669.84**
VRBT-49 x VRBT-50	0.47**	0.11	-0.24**	0.63**	8.08**	2.71**	0.56**	4.39**	23.54**	861.42**
VRBT-49 x VRBT-103	4.22**	3.08**	3.81**	-0.79**	1.7**	2.06**	-0.33**	-1.80**	4.06**	-93.84**
VRBT-49 x VRBT-63	-3.44**	-3.42**	-2.94**	-0.51**	0.36**	0.04	0.03	-3.93**	1.95**	-266.42**
VRBT-49 x VRBT-32	5.89**	6.75**	6.53**	-0.05**	-1.89**	-0.32**	0.77**	-4.63**	0.31**	-343.56**
VRBT-49 x VRBT-6	-4.94**	-5.69**	-7.19**	0.28**	7.23**	0.18**	-0.49**	3.02**	-5.82**	25.05**
VRBT-50 x VRBT-103	-4.72**	-4.64**	-4.66**	0.69**	2.31**	1.38**	-0.26**	4.98**	-0.83**	333.04**
VRBT-50 x VRBT-63	-4.05**	-4.14**	-4.41**	0.17**	5.73**	2.41**	0.29**	3.09**	7.99**	358.42**
VRBT-50 x VRBT-32	0.28**	0.36**	-0.61**	-1.07**	-2.65**	-0.64**	-0.73**	0.69**	-9.95**	-197.05**
VRBT-50 x VRBT-6	-1.22**	-1.08**	-1.33**	-1.06**	-2.36**	-0.17**	0.03	2.18**	0.85**	260.36**
VRBT-103 x VRBT-63	4.7**	3.83**	3.98**	0.51**	-0.85**	0.68**	0.34**	-0.88**	4.97**	9.90**
VRBT-103 x VRBT-32	-7.97**	-8.00**	-7.88**	0.87**	2.04**	1.68**	0.35**	2.72**	5.43**	254.03**
VRBT-103 x VRBT-6	0.86**	1.22**	1.73**	0.33**	-0.38**	2.16**	1.15**	2.44**	8.57**	347.84**
VRBT-63 x VRBT-32	0.70**	0.83**	0.37**	0.25**	-0.30**	1.13**	0.41**	2.40**	4.96**	232.25**
VRBT-63 x VRBT-6	1.20**	0.39**	0.31**	0.58**	2.95**	1.37**	0.71**	1.71**	4.59**	121.42**
VRBT-32 x VRBT-6	-6.8**	-5.78**	-5.88**	0.54**	5.37**	1.30**	0.18**	-2.19**	4.18**	201.12**
SE (sij)	0.0845	0.0901	0.1082	0.0198	0.0695	0.0266	0.0171	0.0474	0.1372	4.0290
SE (sij-sik)	0.1243	0.1325	0.1590	0.0291	0.1022	0.0391	0.0251	0.697	0.2016	5.9230

*, **= Significant at 5% and 1% level of probability, respectively

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